

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2006, 03:52:16 ; Search time 352 Seconds
(without alignments) 139.107 Million cell updates/sec

Title: US-10-601-492-3

Perfect score: 21

Sequence: 1 cgvugagccgguuauucguu 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues 13021146

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New.*

1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---|
| 1 | 18 | 85.7 | 19 | 10 | US-11-101-244-613779 Sequence 613779, |
| 2 | 18 | 85.7 | 19 | 11 | US-11-083-784-613779 Sequence 613779, |
| 3 | 15.2 | 72.4 | 25 | 7 | US-10-934-048A-102729 Sequence 102729, |
| 4 | 14.8 | 70.5 | 25 | 12 | US-11-121-849-216324 Sequence 216324, |
| 5 | 14.2 | 67.6 | 25 | 12 | US-11-121-849-547830 Sequence 547830, |
| 6 | 14 | 66.7 | 25 | 7 | US-10-933-982-75739 Sequence 75739, A |
| 7 | 13.8 | 65.7 | 25 | 7 | US-10-933-982-58238 Sequence 58238, A |
| 8 | 13.8 | 65.7 | 25 | 12 | US-11-121-849-547831 Sequence 547831, |
| 9 | 13.6 | 64.8 | 22 | 8 | US-10-310-914A-236918 Sequence 236918, |
| 10 | 13.6 | 64.8 | 25 | 7 | US-10-932-182A-111151 Sequence 111151, |
| 11 | 13.6 | 64.8 | 25 | 7 | US-10-932-182A-194814 Sequence 194814, |
| 12 | 13.6 | 64.8 | 25 | 7 | US-10-932-182A-111151 Sequence 111151, |
| 13 | 13.6 | 64.8 | 25 | 7 | US-10-932-182A-194814 Sequence 194814, |
| 14 | 13.6 | 64.8 | 25 | 7 | US-10-933-982-92677 Sequence 92677, A |
| 15 | 13.4 | 63.8 | 19 | 10 | US-11-101-244-1290409 Sequence 1290409, |
| 16 | 13.4 | 63.8 | 19 | 10 | US-11-101-244-1306752 Sequence 1306752, |
| 17 | 13.4 | 63.8 | 19 | 11 | US-11-083-784-1390409 Sequence 1290409, |
| 18 | 13.4 | 63.8 | 19 | 11 | US-11-083-784-1306752 Sequence 1306752, |
| 19 | 13.4 | 63.8 | 24 | 12 | US-11-069-908-5819 Sequence 5819, Ap |
| 20 | 13.4 | 63.8 | 25 | 7 | US-10-934-048A-78535 Sequence 78535, A |

ALIGNMENTS

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21 13.4 63.8 25 12 US-11-136-527-137380 Sequence 137380,
22 13.4 63.8 25 12 US-11-136-527-137384 Sequence 137384,
23 13.4 63.8 25 12 US-11-136-527-137385 Sequence 137385,
24 13.4 63.8 25 12 US-11-136-527-137387 Sequence 137387,
25 13.4 63.8 25 12 US-11-136-527-137388 Sequence 137388,
26 13.4 63.8 25 12 US-11-136-527-137389 Sequence 137389,
27 13.4 63.8 25 12 US-11-136-527-137396 Sequence 137396,
28 13.4 63.8 25 12 US-11-136-527-137398 Sequence 137398,
29 13.4 63.8 25 12 US-11-136-527-137398 Sequence 137398,
30 13.2 62.9 22 8 US-10-310-914A-214336 Sequence 214336,
31 13.2 62.9 23 8 US-10-310-914A-214325 Sequence 500143,
32 13.2 62.9 24 8 US-10-310-914A-214325 Sequence 214325,
33 13.2 62.9 25 7 US-10-932-182A-140982 Sequence 140982,
34 13.2 62.9 25 7 US-10-932-182A-140982 Sequence 140982,
35 13.2 62.9 25 7 US-10-934-088-82404 Sequence 82404, A
36 13.2 62.9 25 7 US-10-934-088-25947 Sequence 25947, A
37 13.2 62.9 25 8 US-10-310-914A-116124 Sequence 116124,
38 13.2 62.9 25 12 US-11-121-849-49463 Sequence 49463, A
39 13.2 62.9 25 12 US-11-121-849-193840 Sequence 193840, A
40 13.2 62.9 25 12 US-11-121-849-309450 Sequence 309450,
41 13.2 62.9 25 12 US-11-121-849-178870 Sequence 178870,
42 13.2 62.9 28 8 US-10-310-914A-613834 Sequence 613834,
43 13 61.9 19 10 US-11-083-784-613834 Sequence 613834,
44 13 61.9 19 11 US-11-083-784-613834 Sequence 613834,
45 13 61.9 21 8 US-10-310-914A-385198 Sequence 385198,

RESULT 1
US-11-101-244-613779
; Sequence 613779, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Pharmcon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 613779
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-613779

Query Match 85.7%; Score 18; DB 10; Length 19;
Best local similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUGAGCGGUUUAUCGUGU 21
Db 1 GUGAGCGGUUUAUCGUGU 18

RESULT 2
US-11-083-784-613779
; Sequence 613779, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Pharmcon, Inc.
; APPLICANT: Khvorova, Anastasia

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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134690US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 159191
SOFTWARE: Proprietary
SEQ ID NO: 613779
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-613779

```

| | | | | |
|-----------------------|-----------------|----------------|-----------|------------|
| Query Match | 85.7% | Score 18: | DB 11: | Length 19: |
| Best Local Similarity | 100.0% | Pred. NO. 1.77 | | |
| Matches 18: | Conservative 0: | Mismatches 0: | Indels 0: | Gaps 0: |
| Qy | 4 | GUGAGCGUUU | AUCUGUU | 21 |
| | | | | |
| b | 1 | GUGAGCGUUU | AUCUGUU | 18 |
| | | | | |

```

RESULT 3
US-10-934-048A-102729
: Sequence 102729, Application US/10934048A
: Publication No. US20060051770A1
:
: GENERAL INFORMATION:
:   APPLICANT: Tanya Makeev
:   TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
:   FILE REFERENCE: 3699
:   CURRENT APPLICATION NUMBER: US/10/934, 048A
:   CURRENT FILING DATE: 2004-09-03
:   NUMBER OF SEQ ID NOS: 120855
:   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
:   SEQ ID NO 102729
:
: LENGTH: 25
:
: TYPE: DNA
:
: ORGANISM: S. pombe
: US-10-934-048A-102729

```

| Query Match | Similarity | Score | DB | Length |
|-------------|------------------|-------------------------|------------|----------------------|
| Best | Local | 50.0% | Pred | No 69; |
| Matches | 10; Conservative | 7; | Mismatches | 3; Indels 0; Gaps 0; |
| Qy | 2 | GUUGAGACCGUUUAUCUGU | 21 | |
| | | : : : : : : | | |
| b | 2 | GTGTGAGACCGCTTATCTGAT | 21 | |

```

RESULT 4
US-11-121-849-216324
; Sequence 216324, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

```

```
; SEQ ID NO 216324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-216324
```

| | | | | |
|-----------------------|-------|--------------------|--------|---------------|
| Query Match | 70.5% | Score 14.8; | DB 12; | Length 25; |
| Best Local Similarity | 44.4% | Pred. No. 1.2e+02; | | |
| Matches | 8; | Conservative | 8; | Mismatches 2; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

```

QY      3 UUGGACCGUUUAVUCGU 20
      ::|||:::|:::
Db      5 TGTGACCTTTATATGT 22

```

RESULT 5
US-11-121-849-547830/c
; Sequence 547830, Application US/11121849
; Publication No. US20050272080A1

```

1 AFFILIARY: VOID FORMALIN
2 TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
3 TISSUE
4 TITLE OF INVENTION: Microarrays
5 FILE REFERENCE: 3684.1
6 CURRENT APPLICATION NUMBER: US/11/121,849
7 CURRENT FILING DATE: 2005-05-03
8 PRIOR APPLICATION NUMBER: 60/567,949
9 PRIOR FILING DATE: 2004-05-03
10 NUMBER OF SEQ ID NOS: 673904
11 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
12 SEQ ID NO 547830

```

ORGANISM: Homo sapien
US-11-121-849-547830

| | | | | |
|-----------------------|-------|--------------------|--------|---------------|
| Query Match | 67.6% | Score 14.2; | DB 12; | Length 25; |
| Best Local Similarity | 47.4% | Pred. No. 2.5e+02; | | |
| Matches | 9; | Conservative | 7; | Mismatches 3; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

| | | | |
|----|----|-----------------------|----|
| QY | 2 | GUGUGACCGUUUAUCUGU | 20 |
| | | : : : : : : : : : : : | : |
| Db | 23 | GUGGACTGTTTAACTCT | 5 |

RESULT 6
US-10-933-982-75739/c
; Sequence 75739, Application US/109333982
; Publication No. US20060051769A1

```

1  APPLICANT: Bares, Jennifer
2  TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
3  FILE REFERENCE: 3700
4  CURRENT APPLICATION NUMBER: US/10/933,982
5  CURRENT FILING DATE: 2004-09-03
6  NUMBER OF SEQ. ID NOS: 224976
7  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
8  SEQ ID NO 7539

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-75739

```

| | | | | |
|-----------------------|-----------------|--------------------|-----------|------------|
| Query Match | 66.7% | Score 14; | DB 7; | Length 25; |
| Best Local Similarity | 50.0% | Pred. No. 3.3e+02; | | |
| Matches 7; | Conservative 7; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|----|----------------|----|
| QY | 8 | ACCGUUUAUCUGUU | 21 |
| | | ::: :: :: | |
| Db | 25 | ACCGTTTATCTGTT | 12 |

RESULT 7

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2006, 03:25:27 ; Search time 579 Seconds
(without alignments)
241.725 Million cell updates/sec

Title: US-10-601-492-3

Sequence: 1 cgugugaccgcuuauucugu 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 333246308 residues

Total number of hits satisfying chosen parameters: 3150182

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*
14: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 21 | 100.0 | 21 | 13 | ADRI6250 Human Pab |
| 2 | 19 | 90.5 | 21 | 13 | ADRI6251 Human Pab |
| 3 | 14.4 | 68.6 | 25 | 9 | ACI17033 Human mic |
| 4 | 14.2 | 67.6 | 25 | 9 | ACK23852 Human mic |
| 5 | 14.2 | 67.6 | 25 | 9 | ACK23853 Human mic |
| 6 | 14.2 | 67.6 | 26 | 4 | AAB39289 SNP spect |
| 7 | 13.8 | 65.7 | 23 | 14 | AEB22600 Urokinase |
| 8 | 13.8 | 65.7 | 25 | 14 | ADK69384 Pig Lepet |
| 9 | 13.6 | 64.8 | 25 | 9 | ACI693120 Human mic |
| 10 | 13.4 | 63.8 | 20 | 6 | ABO93101 T. tausch |
| 11 | 13.4 | 63.8 | 25 | 9 | ACI45565 Human mic |
| 12 | 13.2 | 62.9 | 20 | 12 | ADQ13747 DMD regio |
| 13 | 13.2 | 62.9 | 25 | 9 | ACI43660 Human mic |
| 14 | 13.2 | 62.9 | 30 | 2 | AAQ85735 Rat 1 PCR |
| 15 | 13 | 61.9 | 25 | 6 | ABX14218 PCR prime |
| 16 | 13 | 61.9 | 25 | 9 | ACI96769 Human mic |
| 17 | 13 | 61.9 | 26 | 5 | AAI71940 Primer #4 |
| 18 | 13 | 61.9 | 26 | 6 | ABX14214 PCR prime |
| 19 | 13 | 61.9 | 28 | 5 | AAI71943 Primer #6 |

| | | | | | | | | |
|----|------|------|------|----|----------|----------|-----------|-----------|
| C | 20 | 13 | 61.9 | 30 | 3 | AAA14417 | AAA14417 | Conus con |
| C | 21 | 12.8 | 61.0 | 24 | 6 | ABQ03851 | Abq03851 | Oligonuc |
| C | 22 | 12.8 | 61.0 | 25 | 9 | ACK25229 | ACK25229 | Human mic |
| C | 23 | 12.8 | 61.0 | 25 | 9 | ACI27865 | ACI27865 | Human mic |
| 24 | 12.8 | 61.0 | 25 | 9 | ACK03756 | ACK03756 | Human mic | |
| 25 | 12.8 | 61.0 | 25 | 9 | ACI17032 | ACI17032 | Human mic | |
| 26 | 12.8 | 61.0 | 25 | 11 | ADM79618 | Adm79618 | Group B | |
| 27 | 12.8 | 61.0 | 25 | 11 | ADM79681 | Adm79681 | Group B | |
| 28 | 12.8 | 61.0 | 30 | 6 | ABK91929 | Abk91929 | Mouse CDC | |
| 29 | 12.6 | 60.0 | 20 | 12 | ADL15507 | Adl15507 | PCR prim | |
| C | 30 | 12.6 | 60.0 | 20 | 13 | ADT08168 | Adt08168 | CD11b ge |
| C | 31 | 12.6 | 60.0 | 22 | 2 | AAQ21669 | Aaq21669 | MMS compl |
| C | 32 | 12.6 | 60.0 | 22 | 4 | AAE92254 | Aae92254 | Human IGE |
| 33 | 12.6 | 60.0 | 22 | 4 | ADB81044 | Adb81044 | LINE retr | |
| 34 | 12.6 | 60.0 | 24 | 4 | AAF92266 | Aaf92266 | Human IGE | |
| 35 | 12.6 | 60.0 | 25 | 9 | ACK17982 | Ack17982 | Human mic | |
| C | 36 | 12.6 | 60.0 | 25 | 9 | ACI99227 | Act99227 | Human mic |
| C | 37 | 12.6 | 60.0 | 25 | 14 | ADZ87090 | Adz87090 | Human KCN |
| 38 | 12.6 | 60.0 | 26 | 10 | ADF66893 | Adf66893 | PCR prim | |
| 39 | 12.6 | 60.0 | 26 | 12 | ADQ59923 | Adq59923 | Probe mu | |
| C | 40 | 12.6 | 60.0 | 29 | 14 | ADV67359 | Adv67359 | Primer f |
| 41 | 12.4 | 59.0 | 20 | 12 | ADP81789 | Adp81789 | Human MD | |
| 42 | 12.4 | 59.0 | 21 | 13 | AEA91007 | Aea91007 | Human lup | |
| 43 | 12.4 | 59.0 | 25 | 9 | ACI65108 | Act65108 | Human mic | |
| C | 44 | 12.4 | 59.0 | 25 | 9 | ACK17123 | Ack17123 | Human mic |
| 45 | 12.2 | 58.1 | 19 | 6 | AAI40885 | Aai40885 | Gamma toc | |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | ADRI6250 standard; RNA; 21 BP. |
| ID | ADRI6250 |
| XX | |
| AC | ADRI6250; |
| XX | |
| DT | 04-NOV-2004 (first entry) |
| XX | |
| DE | Human Pablo cDNA small interfering RNA (siRNA) molecule #1. |
| XX | |
| KW | -Pablo; sg; small interfering RNA; siRNA; apoptosis; |
| KW | Bcl-XL binding domain; nervous system disorder; neural cell; cell death; |
| KW | Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; |
| KW | spinal muscular atrophy; cancer; neuroprotective; nootropic; |
| KW | antiparkinsonian; muscular; cyostatic. |
| OS | Synthetic. |
| XX | |
| PN | US2004157327-A1. |
| XX | |
| PD | 12-AUG-2004. |
| XX | |
| PF | 23-JUN-2003; 2003US-00601492. |
| XX | |
| PR | 22-OCT-1999; 99US-00425501. |
| PR | 15-MAY-2001; 2001US-00858155. |
| XX | |
| PA | (AMHP) WYETH. |
| XX | |
| PI | Mark RJ, Young KH, Wood AT; |
| XX | |
| DR | WPI, 2004-580273/56. |
| XX | |
| PT | New Pablo polypeptides and encoding nucleic acid molecules useful for |
| PT | modulating apoptosis (i.e. in neural cells), or for diagnosing, |
| PT | preventing or treating disorders associated with cell death, e.g. |
| XX | Alzheimer's disease or cancer. |
| XX | |
| PS | Claim 3; SEQ ID NO 3; 64pp; English. |
| XX | |
| CC | The invention relates to a small interfering RNA (siRNA) molecule that |
| CC | inhibits the expression of a Pablo polypeptide in a eukaryotic cell. The |

CC invention also relates to a method for inhibiting apoptosis in a
CC mammalian cell, comprising administering the siRNA molecule to the cell,
CC a polypeptide comprising an isolated mammalian Bcl-xL binding domain, a
CC method of treating a nervous system disorder in a subject, a method of
CC detecting the presence of Pablo in a cell and a method of identifying a
CC compound that modulates the pro-apoptotic activity of a Bcl-xL binding
CC domain. The composition and methods are useful for modulating apoptosis,
CC particularly in neural cells, as well as for the diagnosis, treatment or
CC prevention of disorders that can benefit from modulation of cell death,
CC e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral
CC sclerosis, spinal muscular atrophy and cancer. These may also be used in
CC drug screening assays or in pharmacogenomics. This sequence represents a
CC small interfering RNA (siRNA) molecule used to inhibit expression of
CC human Pablo CDNA of the invention.

XX Sequence 21 BP; 2 A; 4 C; 6 G; 0 T; 9 U; 0 Other;

Query Match 100.0%; Score 21; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUGUGACCGUUUACUGU 21
|||
DB 1 CGUGUGACCGUUUACUGU 21

RESULT 2

ADRI6251/c
ID ADRI6251 standard; RNA; 21 BP.

AC ADRI6251;

DT 04-NOV-2004 (first entry)

XX Human Pablo cDNA small interfering RNA (siRNA) molecule #2.

DE Pablo; sg; small interfering RNA; siRNA; apoptosis;

KM Bcl-xL binding domain; nervous system disorder; neural cell; cell death;

KM Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;

KM spinal muscular atrophy; cancer; neuroprotective; nootropic;

XX antiparkinsonian; muscular; cyostatic.

OS Synthetic.

XX US2004157327-A1.

PN 12-AUG-2004.

XX 23-JUN-2003; 2003US-00601492.

XX 22-OCT-1999; 99US-00425501.

PR 15-MAY-2001; 2001US-00858155.

XX (AMHP) WYETH.

PA Mark RJ, Young KH, Wood AT;

PI WPI; 2004-580273/56.

DR New Pablo polypeptides and encoding nucleic acid molecules useful for

XX PT modulating apoptosis (i.e. in neural cells), or for diagnosing,

PT preventing or treating disorders associated with cell death, e.g.

XX PT Alzheimer's disease or cancer.

XX Claim 3; SEQ ID NO 4; 64pp; English.

CC The invention relates to a small interfering RNA (siRNA) molecule that
CC inhibits the expression of a Pablo polypeptide in a eukaryotic cell. The
CC invention also relates to a method for inhibiting apoptosis in a
CC mammalian cell, comprising administering the siRNA molecule to the cell,
CC a polypeptide comprising an isolated mammalian Bcl-xL binding domain, a
CC method of treating a nervous system disorder in a subject, a method of
CC detecting the presence of Pablo in a cell and a method of identifying a

CC compound that modulates the pro-apoptotic activity of a Bcl-xL binding
CC domain. The composition and methods are useful for modulating apoptosis,
CC particularly in neural cells, as well as for the diagnosis, treatment or
CC prevention of disorders that can benefit from modulation of cell death,
CC e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral
CC sclerosis, spinal muscular atrophy and cancer. These may also be used in
CC drug screening assays or in pharmacogenomics. This sequence represents a
CC small interfering RNA (siRNA) molecule used to inhibit expression of
CC human Pablo CDNA of the invention.

XX Sequence 21 BP; 7 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 90.5%; Score 19; DB 13; Length 21;
Best Local Similarity 63.2%; Pred. No. 5.9;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUGUGACCGUUUACUG 19
|||
DB 19 CGUGUGACCGUUUACUG 1

RESULT 3

ACII17033
ID ACII17033 standard; DNA; 25 BP.

XX ACII17033;

DT 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 17024.

DE EST; sg; probe; expressed sequence tag; microarray; gene expression;

KM genetic variation; diallelic marker; polymorphism; human;

KM cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFIMETRIX INC.

XX Miltmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in

XX Southern, Northern or dot-blot hybridization to identify or detect the

XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 17024; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic

XX acid probes including one of 2,018,500 fully defined sequences, or its

XX perfect match, antisense match or antisense mismatch.

XX Also disclosed is a method of gene expression analysis. The array is used

XX in monitoring gene expression levels by hybridisation to a DNA library,

XX in analysis of genetic variation or in hybridisation of tag-labelled

XX compounds. The nucleic acid probes are specifically designed for analysis

XX of at least one target sequence. The method of analysis comprises

XX hybridising at least one or more nucleic acids to at least two or more

XX nucleic acid probes and detecting the hybridisation. The nucleic acid

XX probes are attached to a solid support. The analysis comprises monitoring

XX gene expression levels, identifying diallelic markers or polymorphisms,

XX or family members of a gene and a cross-species comparison. Each of the

XX nucleic acids further comprises a tag sequence. The array of nucleic acid

XX probes is useful in in situ hybridisation, in Southern, Northern or dot-

XX blot hybridisation to identify or detect the sequence or specific